

## SEARCH REQUEST FORM

Scientific and Technical Information Center

CATE

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 8/15/02  
 Art Unit: 1635 Phone Number 305-5220 Serial Number: 09/522,278  
 Mail Box and Bldg/Room Location: 11003 Results Format Preferred (circle): PAPER DISK E-MAIL

11e12

If more than one search is submitted, please prioritize searches in order of need.

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Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Delivery of Substances to CellsInventors (please provide full names): Jane et alEarliest Priority Filing Date: 2/14/01

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search Sig ID No 12.

— Size limit to 50AA

Unlimited search.

Edward Han  
 Technical Info. Specialist  
 STIC/Biotech  
 CMI 6B02 Tel: 305-9203

Interference + Regular  
 Dto Bas.  
 Thanks.

pat 12

## STAFF USE ONLY

Searcher: \_\_\_\_\_

## Type of Search

## Vendors and cost where applicable

NA Sequence (#) \_\_\_\_\_ STN \_\_\_\_\_

AA Sequence (#) 2 Dialog \_\_\_\_\_

Structure (#) \_\_\_\_\_ Questel/Orbit \_\_\_\_\_

Bibliographic \_\_\_\_\_ Dr. Link \_\_\_\_\_

Litigation \_\_\_\_\_ Lexis/Nexis \_\_\_\_\_

Fulltext \_\_\_\_\_ Sequence Systems \_\_\_\_\_ PO

Patent Family \_\_\_\_\_ WWW/Internet \_\_\_\_\_

Other \_\_\_\_\_ Other (specify) \_\_\_\_\_

PTO-1590 (8-01)

Copyright (c) 1993 - 2000 Compugen Ltd.	GenCore version 4.5									
OM protein - protein search, using sw model										
Run on: August 28, 2002, 12:23:41 ; Search time 30.25 Seconds	(Without alignments)									
Scoring table: BLOSUM62	1721.371 Million cell updates/sec									
Title: US-09-522-278B-12										
Perfect score: 1561										
Sequence: 1 MTSRRRSVSKGGPREVPRDYE..... PTERPAPAPARSASRPRRPVE 301										
Scoring table: Gppop 10.0 , Gapext 0.5										
Searched: 562222 seqs, 17294929 residues										
Total number of hits satisfying chosen parameters: 562222										
Minimum DB seq length: 0										
Maximum DB seq length: 2000000000										
Post-processing: Minimum Match 0%										
Maximum Match 100%										
Listing first 45 summaries										
Database: SPREMBL_19										
1: sp_archaea:*										
2: sp_bacteria:*										
3: sp_fungi:*										
4: sp_invertebrate:*										
5: sp_mammal:*										
6: sp_mmc:*										
7: sp_organelle:*										
8: sp_phase:*										
9: sp_plant:*										
10: sp_rabbit:*										
11: sp_rat:*										
12: sp_virus:*										
13: sp_vertebrate:*										
14: sp_unclassified:*										
15: sp_rvirus:*										
16: sp_bacteria:*										
17: sp_archeap:*										
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.										
SUMMARIES										
Result No.	Score	Query Match Length	DB ID	Description	RESULT ID	1	PRT:	300 AA.	ALIGNMENTS	
1	1014.5	65.0	300	P89468 herpes simp	P89468	PRELIMINARY:				
2	270.5	11.3	304	03923 equine herp	AC	P8968:				
3	228	14.6	301	03925 coracophteric	AC	01-MAY-1997 (TREMBL: 03, created)	DT			
4	210	13.5	12	098205 mare's dis	AC	01-MAY-1997 (TREMBL: 03, last sequence update)	DT			
5	210	13.5	249	098318 mare's dis	AC	01-JUN-2001 (TREMBL: 19, last annotation update)	DT			
6	207	13.3	241	098247 turkey herp	AC	TEGMENT PROTEIN.	DE			
7	198	12.7	12	098247 gallid herp	AC	UL40.	GN			
8	168.5	10.8	389	09842 herpes simplex	AC	Herpes simplex virus (type 2).	OS			
9	168.5	10.8	441	098685 herpes simplex	AC	Viruses: dsDNA, viruses, no RNA stage; Herpesviridae;	OC			
10	153	9.8	252	12 Q9DWG9	AC	Alphaherpesvirinae; Simplexvirus.	OC			
11	149.5	9.6	956	4 Q9UQ39	AC	NCBA_TAXID-10310;	OC			
12	149.5	9.6	2752	4 Q9UQ35	AC	[1]	RN		SEQUENCE FROM N. A.	
13	149.5	9.6	3122	12 P89459	AC	STRAIN-HG52;	RC			
14	148	9.5	266	12 098686	AC	MEDLINE-92113549; PubMed-1662697;	RC			
15	146.5	9.4	16	09874	AC	McGoch D.J., Cunningham C., McIntyre G., Dolan A.;	RC			
16	146.5	9.4	1343	4 Q9H7N4	AC	*Comparative sequence analysis of the long repeat regions and adjoining parts of the long unique regions in the genomes of herpes	RT			